ep
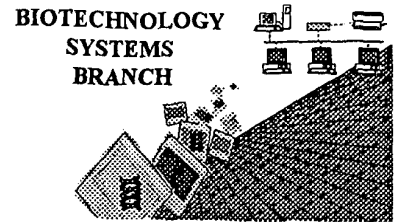
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___*10/629,266*___
Source: ___*OIPE*___
Date Processed by STIC: ___*8/11/2003*___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission **User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry directly to:**
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
            Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/629,266_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences (OLD RULES)

Sequence(s)____missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.

8____Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10____Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 08/11/2003
PATENT APPLICATION: **US/10/629,266**   TIME: 13:40:23

     Input Set : **A:\U0158.GENE-SEQUENCE-LIST.DOC.txt**
     Output Set: **N:\CRF4\08112003\J629266.raw**

```
    3 <110> APPLICANT: Zhang, Yeyan
    4        Wilson, C. Ron
    5        Craft, David L.
    6        Eirich, L. Dudley
    7        Frayer, Robert
    9 <120> TITLE OF INVENTION: USE OF POX4 PROMOTER TO INCREASE GENE EXPRESSION IN Candida
   10        tropicalis
   12 <130> FILE REFERENCE: U0158 OS/OAPT (1010-93)
```
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/629,266
C--> 14 <141> CURRENT FILING DATE: 2003-07-29
```
   14 <150> PRIOR APPLICATION NUMBER: 60/401,212
   15 <151> PRIOR FILING DATE: 2002-08-05
   17 <160> NUMBER OF SEQ ID NOS: 34
   19 <170> SOFTWARE: PatentIn version 3.2
```

ERRORED SEQUENCES

Does Not Comply
Corrected Diskette Needed

```
  417 <210> SEQ ID NO: 34
  418 <211> LENGTH: 23
  419 <212> TYPE: PRT
  420 <213> ORGANISM: Artificial Sequence
  422 <220> FEATURE:
  423 <223> OTHER INFORMATION: peptide
  425 <400> SEQUENCE: 34
  427 Ser Glu Asp Lys Ala Ala Glu Leu Val Lys Ser Trp Lys Val Gln Asn
  428 1               5                   10                  15
  431 Arg Tyr Gln Glu Asp Val Trp
  432                 20
E--> 438 9
```
insufficient explanation – give source of genetic material (see item 11 on Error Summary Sheet)

delete

VERIFICATION SUMMARY   DATE: 08/11/2003
PATENT APPLICATION: **US/10/629,266**   TIME: 13:40:24

Input Set : **A:\U0158.GENE-SEQUENCE-LIST.DOC.txt**
Output Set: **N:\CRF4\08112003\J629266.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:438 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:34

STATISTICS SUMMARY   DATE: 08/11/2003
PATENT APPLICATION: **US/10/629,266**   TIME: 13:40:24

Input Set : **A:\U0158.GENE-SEQUENCE-LIST.DOC.txt**
Output Set: **N:\CRF4\08112003\J629266.raw**

Application Serial Number: US/10/629,266
Alpha or Numeric or Xml: Numeric
Application Class:
Application File Date: 07-29-2003
Art Unit: OIPE
Software Application: PatentIN3.2
Total Number of Sequences: 34
Total Nucleotides: 817
Total Amino Acids: 23
Number of Errors: 1
Number of Warnings: 0
Number of Corrections: 2

MESSAGE SUMMARY

270 C: 1 (Current Application Number differs)
271 C: 1 (Current Filing Date differs)
332 E: 1 ((32) Invalid/Missing Amino Acid Numbering)